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<223> Antisense Oligonucleotide

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<210> 168

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SEQUENCE LISTING

<110> Hong Zhang
Andrew T. Watt

<120> ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION

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gag cag atc atg aag aca ggg gcc ctt ttg ctt cag ggt ttc atc cag	96
Glu Gln Ile Met Lys Thr Gly Ala Leu Leu Leu Gln Gly Phe Ile Gln	
20 25 30	
gat cga gca ggg cga atg ggg ggg gag gca ccc gag ctg gcc ctg gac	144
Asp Arg Ala Gly Arg Met Gly Gly Glu Ala Pro Glu Leu Ala Leu Asp	
35 40 45	
ccg gtg cct cag gat gcg tcc acc aag aag ctg agc gag tgt ctc aag	192
Pro Val Pro Gln Asp Ala Ser Thr Lys Lys Leu Ser Glu Cys Leu Lys	
50 55 60	
cgc atc ggg gac gaa ctg gac agt aac atg gag ctg cag agg atg att	240
Arg Ile Gly Asp Glu Leu Asp Ser Asn Met Glu Leu Gln Arg Met Ile	
65 70 75 80	
gcc gcc gtg gac aca gac tcc ccc cga gag gtc ttt ttc cga gtg gca	288
Ala Ala Val Asp Thr Asp Ser Pro Arg Glu Val Phe Phe Arg Val Ala	
85 90 95	
gct gac atg ttt tct gac ggc aac ttc aac tgg ggc cgg gtt gtc gcc	336
Ala Asp Met Phe Ser Asp Gly Asn Phe Asn Trp Gly Arg Val Val Ala	
100 105 110	
ctt ttc tac ttt gcc agc aaa ctg gtg ctc aag gcc ctg tgc acc aag	384
Leu Phe Tyr Phe Ala Ser Lys Leu Val Leu Lys Ala Leu Cys Thr Lys	
115 120 125	
gtg ccg gaa ctg atc aga acc atc atg ggc tgg aca ttg gac ttc ctc	432
Val Pro Glu Leu Ile Arg Thr Ile Met Gly Trp Thr Leu Asp Phe Leu	

130 135 140

cgg gag cgg ctg ttg ggc tgg atc caa gac cag ggt ggt tgg gtg aga 480
Arg Glu Arg Leu Leu Gly Trp Ile Gln Asp Gln Gly Gly Trp Val Arg
145 150 155 160

ctc ctc aag cct cct cac ccc cac cac cgc gcc ctc acc acc gcc cct 528
Leu Leu Lys Pro Pro His Pro His His Arg Ala Leu Thr Thr Ala Pro
165 170 175

gcc cca ccg tcc ctg ccc ccc gcc act cct ctg gga ccc tgg gcc ttc 576
Ala Pro Pro Ser Leu Pro Pro Ala Thr Pro Leu Gly Pro Trp Ala Phe
180 185 190

tgg agc agg tca cag tgg tgc cct ctc ccc atc ttc aga tca tca gat 624
Trp Ser Arg Ser Gln Trp Cys Pro Leu Pro Ile Phe Arg Ser Ser Asp
195 200 205

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18

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<210> 8

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<210> 9
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1 5 10 15

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Glu Gln Ile Met Lys Thr Gly Ala Phe Leu Leu Gln Gly Phe Ile Gln
20 25 30

gat cga gca ggg agg atg gct ggg gag aca cct gag ctg acc ttg gag 144
Asp Arg Ala Gly Arg Met Ala Gly Glu Thr Pro Glu Leu Thr Leu Glu
35 40 45

cag ccg ccc cag gat gcg tcc acc aag aag ctg agc gag tgt ctc cgg 192
Gln Pro Pro Gln Asp Ala Ser Thr Lys Lys Leu Ser Glu Cys Leu Arg
50 55 60

cga att gga gat gaa ctg gat agc aat atg gag ctg cag agg atg att 240
Arg Ile Gly Asp Glu Leu Asp Ser Asn Met Glu Leu Gln Arg Met Ile
65 70 75 80

gct gac gtg gac acg gac tcc ccc cga gag gtc ttc ttc cgg gtg gca 288
 Ala Asp Val Asp Thr Asp Ser Pro Arg Glu Val Phe Phe Arg Val Ala
 85 90 95

gct gac atg ttt gct gat ggc aac ttc aac tgg ggc cgc gtg gtt gcc 336
 Ala Asp Met Phe Ala Asp Gly Asn Phe Asn Trp Gly Arg Val Val Ala
 100 105 110

ctc ttc tac ttt gct agc aaa ctg gtg ctc aag gcc ctg tgc act aaa 384
 Leu Phe Tyr Phe Ala Ser Lys Leu Val Leu Lys Ala Leu Cys Thr Lys
 115 120 125

gtg ccc gag ctg atc aga acc atc atg ggc tgg aca ctg gac ttc ctc 432
 Val Pro Glu Leu Ile Arg Thr Ile Met Gly Trp Thr Leu Asp Phe Leu
 130 135 140

cgt gag cgg ctg ctt gtc tgg atc caa gac cag ggt ggc tgg gaa ggc 480
 Arg Glu Arg Leu Leu Val Trp Ile Gln Asp Gln Gly Gly Trp Glu Gly
 145 150 155 160

ctc ctc tcc tac ttc ggg acc ccc aca tgg cag aca gtg acc atc ttt 528
 Leu Leu Ser Tyr Phe Gly Thr Pro Thr Trp Gln Thr Val Thr Ile Phe
 165 170 175

gtg gct gga gtc ctc acc gcc tcg ctc acc atc tgg aag aag atg ggc 576
 Val Ala Gly Val Leu Thr Ala Ser Leu Thr Ile Trp Lys Lys Met Gly
 180 185 190

tga 579

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22

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<223> PCR Primer

<400> 12

gagacactcg ctcagcttct tg

22

<210> 13

<211> 19

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<220>

<223> PCR Probe

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<210> 14

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer

<400> 14

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<210> 15

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> PCR Primer

<400> 15

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<210> 16

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Probe

<400> 16

aaggccgaga atgggaagct tgtcatc

27

<210> 17

<211> 677

<212> DNA

<213> Homo sapiens

<220>

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<221> CDS

<222> (1)...(495)

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1 5 10 15

48

gag cag atc atg aag aca ggg gcc ctt ttg ctt cag ggt ttc atc cag
Glu Gln Ile Met Lys Thr Gly Ala Leu Leu Leu Gln Gly Phe Ile Gln

96

20

25

30

gat cga gca ggg cga atg ggg ggg gag gca ccc gag ctg gcc ctg gac 144
Asp Arg Ala Gly Arg Met Gly Gly Glu Ala Pro Glu Leu Ala Leu Asp
35 40 45

ccg gtg cct cag gat gcg tcc acc aag aag ctg agc gag tgt ctc aag 192
Pro Val Pro Gln Asp Ala Ser Thr Lys Lys Leu Ser Glu Cys Leu Lys
50 55 60

cgc atc ggg gac gaa ctg gac agt aac atg gag ctg cag agg atg att 240
Arg Ile Gly Asp Glu Leu Asp Ser Asn Met Glu Leu Gln Arg Met Ile
65 70 75 80

gcc gcc gtg gac aca gac tcc ccc cga gag gtc ttt ttc cga gtg gca 288
Ala Ala Val Asp Thr Asp Ser Pro Arg Glu Val Phe Phe Arg Val Ala
85 90 95

gct gac atg ttt tct gac ggc aac ttc aac tgg ggc cgg gtt gtc gcc 336
Ala Asp Met Phe Ser Asp Gly Asn Phe Asn Trp Gly Arg Val Val Ala
100 105 110

ctt ttc tac ttt gcc agc aaa ctg gtg ctc aag gct ggc gtg aaa tgg 384
Leu Phe Tyr Phe Ala Ser Lys Leu Val Leu Lys Ala Gly Val Lys Trp
115 120 125

cgt gat ctg ggc tca ctg caa cct ctg cct cct ggg ttc aag cga ttc 432
Arg Asp Leu Gly Ser Leu Gln Pro Leu Pro Pro Gly Phe Lys Arg Phe
130 135 140

acc tgc ctc agc atc cca agg agc tgg gat tac agg ccc tgt gca cca 480
Thr Cys Leu Ser Ile Pro Arg Ser Trp Asp Tyr Arg Pro Cys Ala Pro
145 150 155 160

agg tgc cgg aac tga tcagaacat catgggctgg acattggact tcctccggga 535
Arg Cys Arg Asn
165

gcggctgttg ggctggatcc aagaccaggg tggttgggac ggctcctct cctacttttg 595

gacgcccacg tggcagaccg tgaccatctt tgtggcggga gtgctcaccg cctcgtcac 655

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1 5 10 15	

gag cag atc atg aag aca ggg gcc ctt ttg ctt cag ggt ttc atc cag	96
Glu Gln Ile Met Lys Thr Gly Ala Leu Leu Leu Gln Gly Phe Ile Gln	
20 25 30	

gat cga gca ggg cga atg ggg ggg gag gca ccc gag ctg gcc ctg gac	144
Asp Arg Ala Gly Arg Met Gly Gly Glu Ala Pro Glu Leu Ala Leu Asp	
35 40 45	

ccg gtg cct cag gat gcg tcc acc aag aag ctg agc gag tgt ctc aag	192
Pro Val Pro Gln Asp Ala Ser Thr Lys Lys Leu Ser Glu Cys Leu Lys	
50 55 60	

cgc atc ggg gac gaa ctg gac agt aac atg gag ctg cag agg atg att	240
Arg Ile Gly Asp Glu Leu Asp Ser Asn Met Glu Leu Gln Arg Met Ile	
65 70 75 80	

gcc gcc gtg gac aca gac tcc ccc cga gag gtc ttt ttc cga gtg gca	288
Ala Ala Val Asp Thr Asp Ser Pro Arg Glu Val Phe Phe Arg Val Ala	
85 90 95	

gct gac atg ttt tct gac ggc aac ttc aac tgg ggc cgg gtt gtc gcc	336
Ala Asp Met Phe Ser Asp Gly Asn Phe Asn Trp Gly Arg Val Val Ala	
100 105 110	

ctt ttc tac ttt gcc agc aaa ctg gtg ctc aag gcc ctg tgc acc aag	384
Leu Phe Tyr Phe Ala Ser Lys Leu Val Leu Lys Ala Leu Cys Thr Lys	
115 120 125	

gtg ccg gaa ctg atc aga acc atc atg ggc tgg aca ttg gac ttc ctc	432
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Val Pro Glu Leu Ile Arg Thr Ile Met Gly Trp Thr Leu Asp Phe Leu
130 135 140

cgg gag cgg ctg ttg ggc tgg atc caa gac cag ggt ggt tgg gac ggc 480
Arg Glu Arg Leu Leu Gly Trp Ile Gln Asp Gln Gly Gly Trp Asp Gly
145 150 155 160

ctc ctc tcc tac ttt ggg acg ccc acg tgg cag acc gtg acc atc ttt 528
Leu Leu Ser Tyr Phe Gly Thr Pro Thr Trp Gln Thr Val Thr Ile Phe
165 170 175

gtg gcg gga gtg ctc acc gcc tcg ctc acc atc tgg aag aag atg ggc 576
Val Ala Gly Val Leu Thr Ala Ser Leu Thr Ile Trp Lys Lys Met Gly
180 185 190

tga 579

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gggaggggtg gggattgggg gacatgggca tttttcttac ttttgtaatt attggggggt 180

gtggggaaaa gtggtcttga gggggtaata aacctccttc gggacccaaa aaaaaaaaaa 240

aaaaaaaaaa aaaaaaaaaa aaa 263

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gcagtgagcc cagggatgct cccctcaga tctgtgagga cctggggatc gtggtatcaa 180
ccccctgcag tggcccagtg accacagagg gcatggagag agatggctgt gcactgggtg 240
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tcacgtgcag ggggtgaagta aagtgggcag agtgatttag cagagtggac aggaaagatt 420
tctatTTTTT tttttttttt ttttgagatg gagttttgct cttgttgccc aggcttgagt 480
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gtaaggggag ccacagaggg tcaggggggg ggcagttgga gagtaacaat cttgttgaca 180
atTTTtatgtt ttatatTTat ttggaagacg gatttgctta tctccaaggc tggcgtgaaa 240
tggcgtgac tgggctcact gcaacctctg cctcctgggt tcaagcgatt cacctgcctc 300
agcatcccaa ggagctggga ttacaggtgc ctgccaccac accagctaa tttttgtatt 360

tatttatttt agagatggag ttttgccttt gttgtgcca ggctggagtg caatggcgca 420
acctcggttc actgcaacct ccgcctcccg ggttcaagca attctcctgc ctcagactcc 480
caagtagctg ggattacagg catgtgccac cacgcccggg aattttgtat ttttagtaga 540
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ctgccttggc ctccccaaag tgctgggatt acaggcatga gccgccgcac ctggccatgt 660
ttacaatttt tgaagccgat tcaattgtgg gtggcagaaa ttttgagggg aggcaaagaa 720
ttgacaaagg aggtttgggg ccactatctc aggcagtggg gacaaggttc agtccctaac 780
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1 5 10 15

gag cag ggc gaa tgg ggg ggg agg cac ccg agc tgg ccc tgg acc cgg 96
Glu Gln Gly Glu Trp Gly Gly Arg His Pro Ser Trp Pro Trp Thr Arg
20 25 30

tgc ctc agg atg cgt cca cca aga agc tga 126
Cys Leu Arg Met Arg Pro Pro Arg Ser
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<223> Antisense Oligonucleotide

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<210> 25

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Antisense Oligonucleotide

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<210> 26

<211> 20

<212> DNA

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<223> Antisense Oligonucleotide

<400> 26

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<212> DNA

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<210> 28

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<211> 20

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<400> 29

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<210> 31
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<210> 32
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<210> 36

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<223> Antisense Oligonucleotide

<400> 36

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<210> 37

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<223> Antisense Oligonucleotide

<400> 37

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<210> 38

<211> 20

<212> DNA

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tcctggatga aaccctgaag

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<210> 39

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<400> 39

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<210> 40
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<210> 42
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<210> 43
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<400> 43

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<210> 44

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<212> DNA

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<223> Antisense Oligonucleotide

<400> 44

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<210> 45

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Antisense Oligonucleotide

<400> 45

cttcttggtg gacgcatcct

20

<210> 46

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Antisense Oligonucleotide

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<210> 47

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Antisense Oligonucleotide

<400> 47

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<210> 48

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Antisense Oligonucleotide

<400> 48

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<210> 49

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Antisense Oligonucleotide

<400> 49

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<210> 50

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Antisense Oligonucleotide

<400> 50

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<210> 51

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<223> Antisense Oligonucleotide

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<223> Antisense Oligonucleotide

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<223> Antisense Oligonucleotide

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<210> 57
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<400> 57
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<210> 58
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<400> 58
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20

<210> 59
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